```
cons.aa          G G  G V                A K          E
hTGFBR-II   LDTLVGKGRFAEVYKAKLKQNTSEQFETVAVKIFPYDHYASWKDRKDIFSDINLKHENILQF
mActR-IIB   LLEIKARGRFGCVWKAQLMN------DFVAVKIKPLQDKQSWQSEREIFSTPGMKHENLLQF
mActR-II    LLEVKARGRFGCVWKAQLLN------EYVAVKIFPIQDKQSWQNEYEVYSIPGMKHENILQF
daf-1       LTGRVGSGRFGNVSRGDYRG------EAVAVKVFNAIDEPAFHKEIEIFETRMLRHPNVLRY
subdomains          I                        II        III           IV

hTGFBR-II   LTAEERKTELGKQYWLITAFHAKGNLQEYLTRHVISWEDLRNVGSSLARGLSHLHSDHTP-C
mActR-IIB   IAAEKRGSNLEVELWLITAFHDKGSLIDYLKGNIITWNELCHVAETMSRGISYLHEDVPWCR
mActR-II    IGAEKRGTSVDVDLWLITAFHEKGSLSDFLKANVVSWNELCHIAETMARGLAYLHEDIPGLK
daf-1       IGSDRVDTGFVTELWLVIEYHPSGSLHDFLLENTVNIETYYNLMRSTASGLAFLHNQIGGSK
subdomains                           V                        VI-A

cons.aa               DLK  N            DFG
hTGFBR-II   -GRPKMPIVHRDLKSSNILVKNDLTCCLCDFGLSLRL---GPYSSVDDLANSGQVGTARYMAP
mActR-IIB   GEGHKPSIAHRDFKSKNVLLKSDLTAVLADFGLAVRF---EPGKPPGD--THGQVGTRRYMAP
mActR-II    -DGHKPAISHRDIKSKNVLLKNNLTACIADFGLALKF---EAGKSAGD--THGQVGTRRYMAP
daf-1       -ESNKPAMAHRDIKSKNIMYKNDLTCAIGDLGLSLSKPEDAASDIIAN--ENYKCGTVRYLAP
subdomains      VI-B                      VII                    VIII
```

Fig. 1

a.a C C E G N M C
5′ GCGGATCCTGTTGTGAAGGNAATATGTG 3′ Fig. 2A
BAMHI C C G C

a.a V A V K I F
5′ GCGGATCCGTCGCAGTCAAAATTTT 3′ Fig. 2B
BamHI G C G G C
T T T A

a.a R D I K S K N
5′ GCGGATCCGCGATATTAAAAGCAA 3′ Fig. 2C
BAMHI A C C GTCT
G A

a.a E P A M Y
5′ CGGAATTCTGGTGCCATATA Fig. 2D
EcoRI G G G
A A

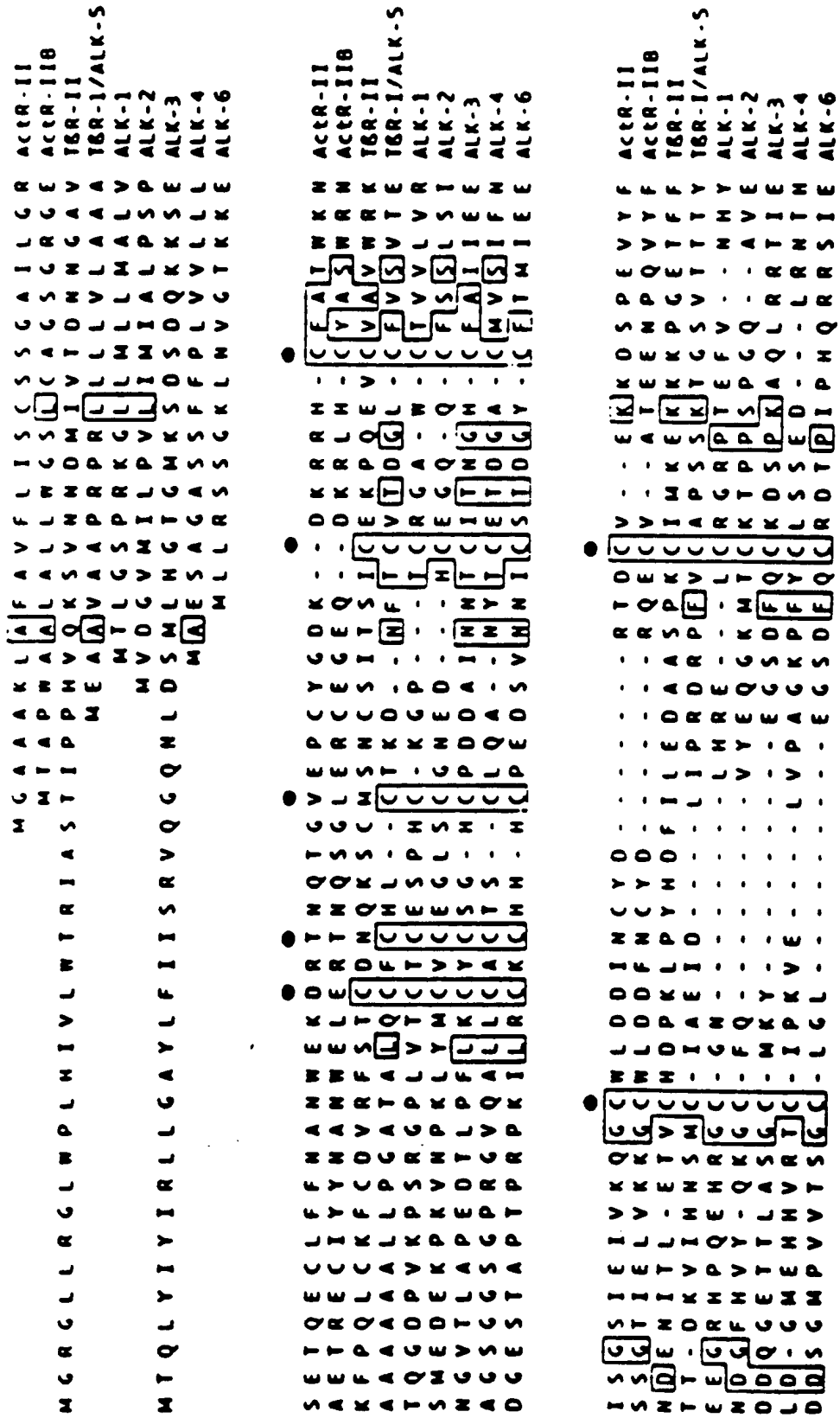

Fig.3

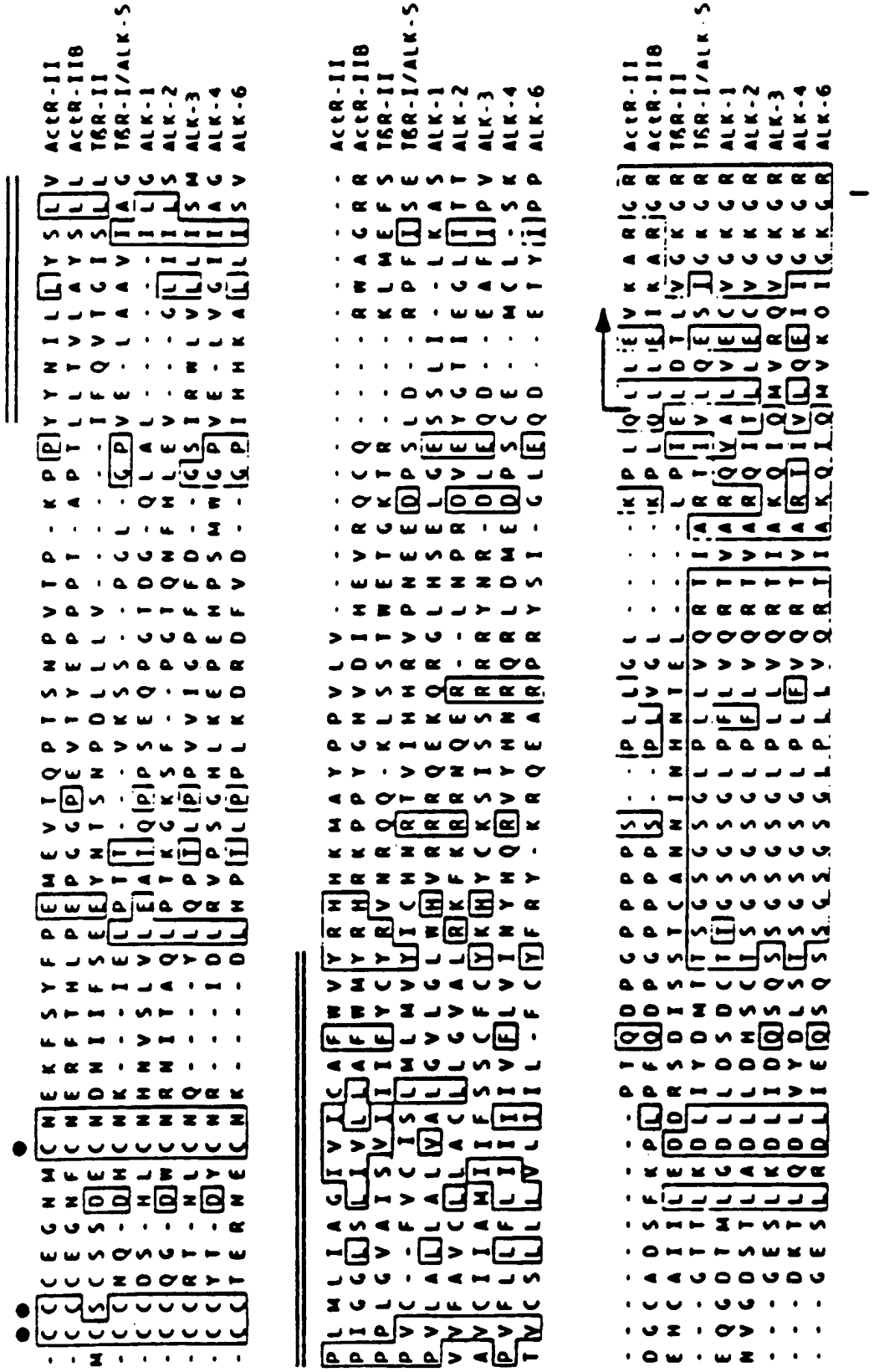

Fig. 3 contd.

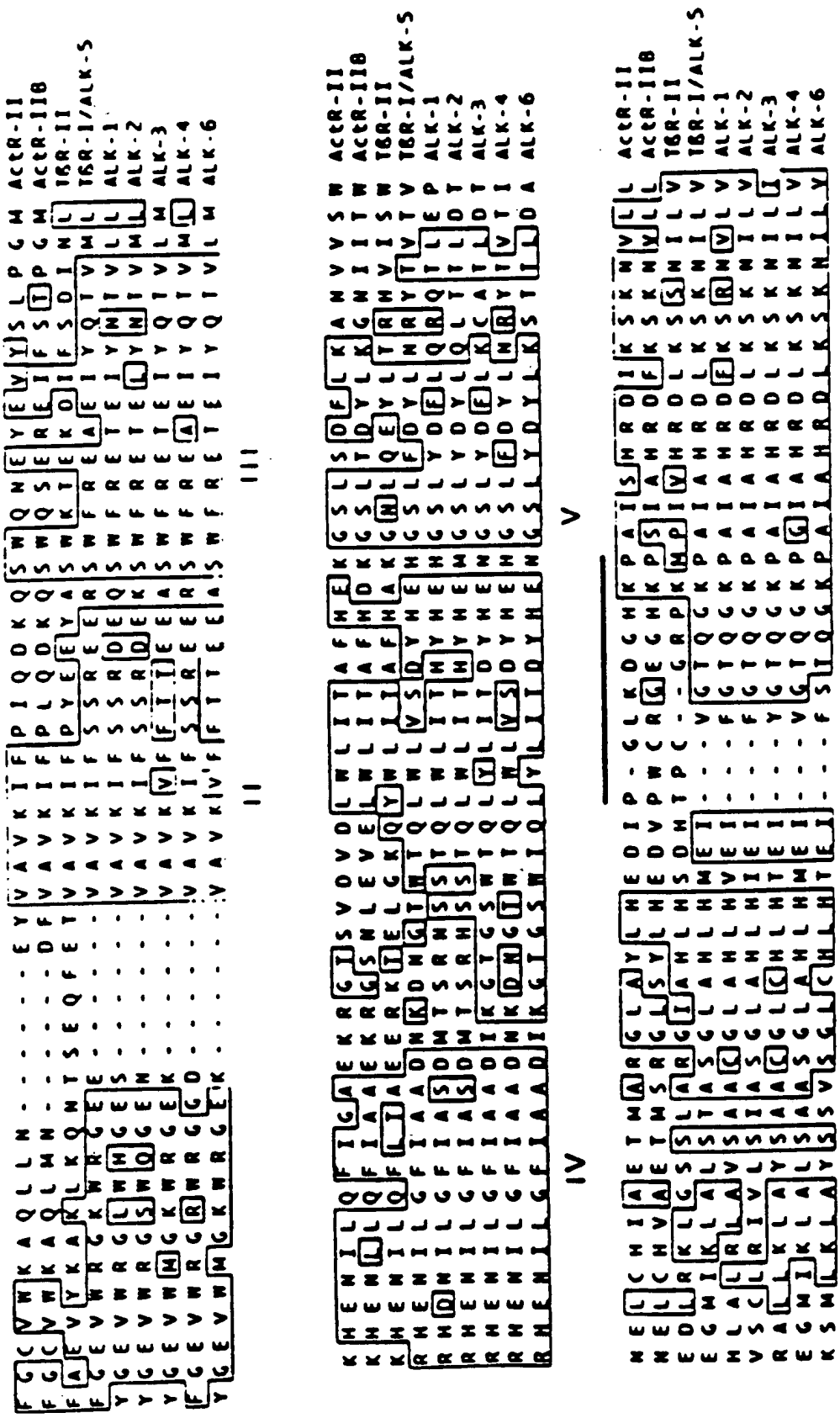
ActR-II
ActR-IIB
TGR-II
TGR-I/ALK-5
ALK-1
ALK-2
ALK-3
ALK-4
ALK-6
I
II
III
IV
V
VIA
VIB

Fig. 3 contd.

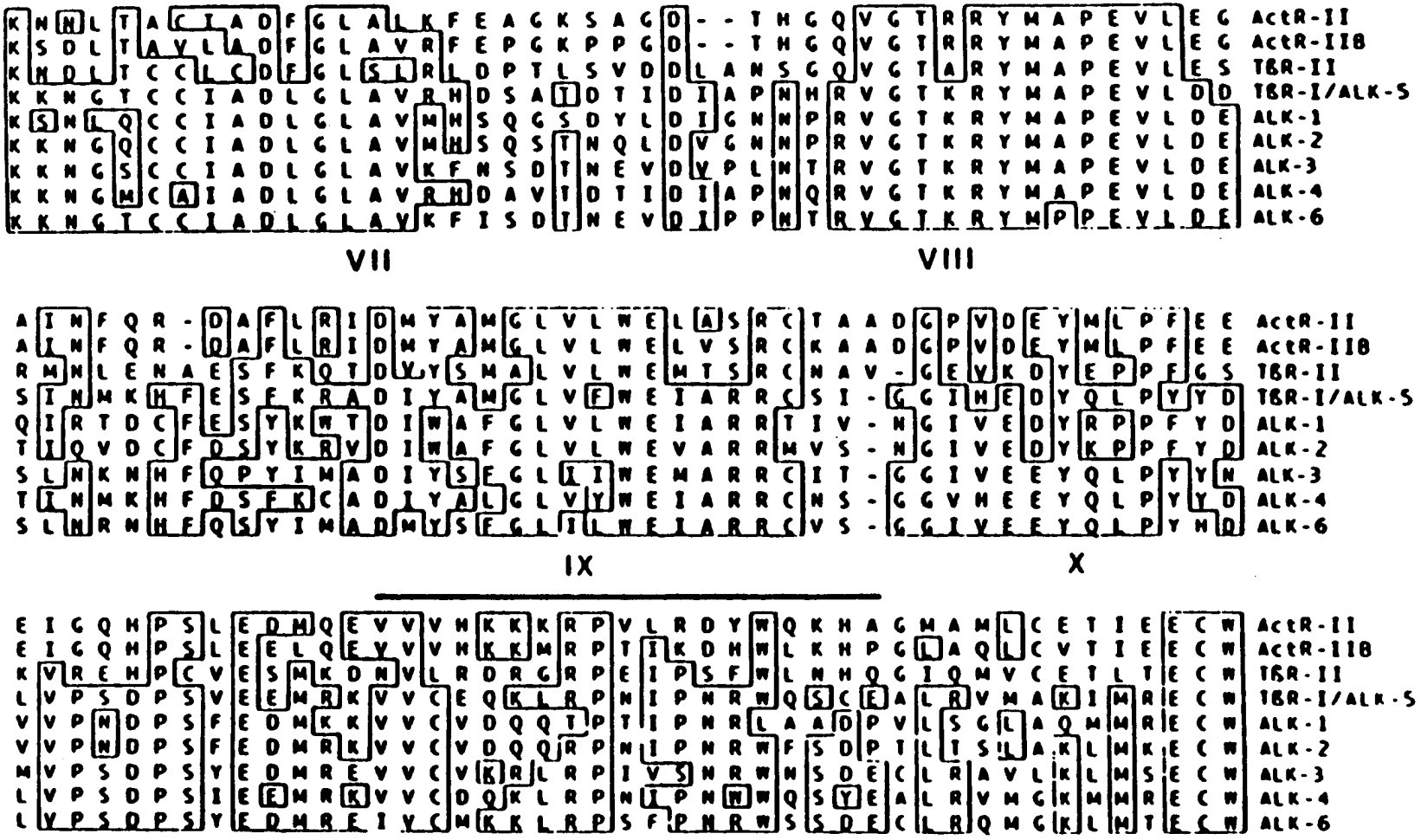

Fig. 3 contd.

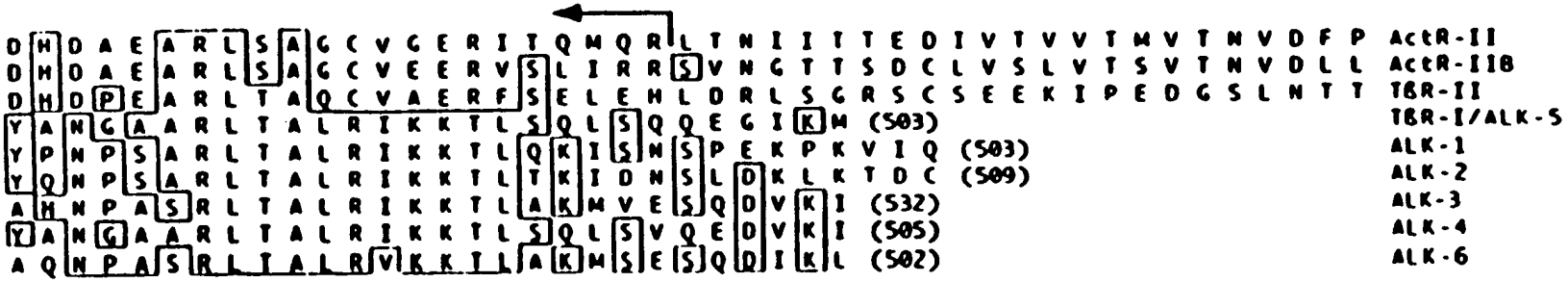

Fig. 3 contd.

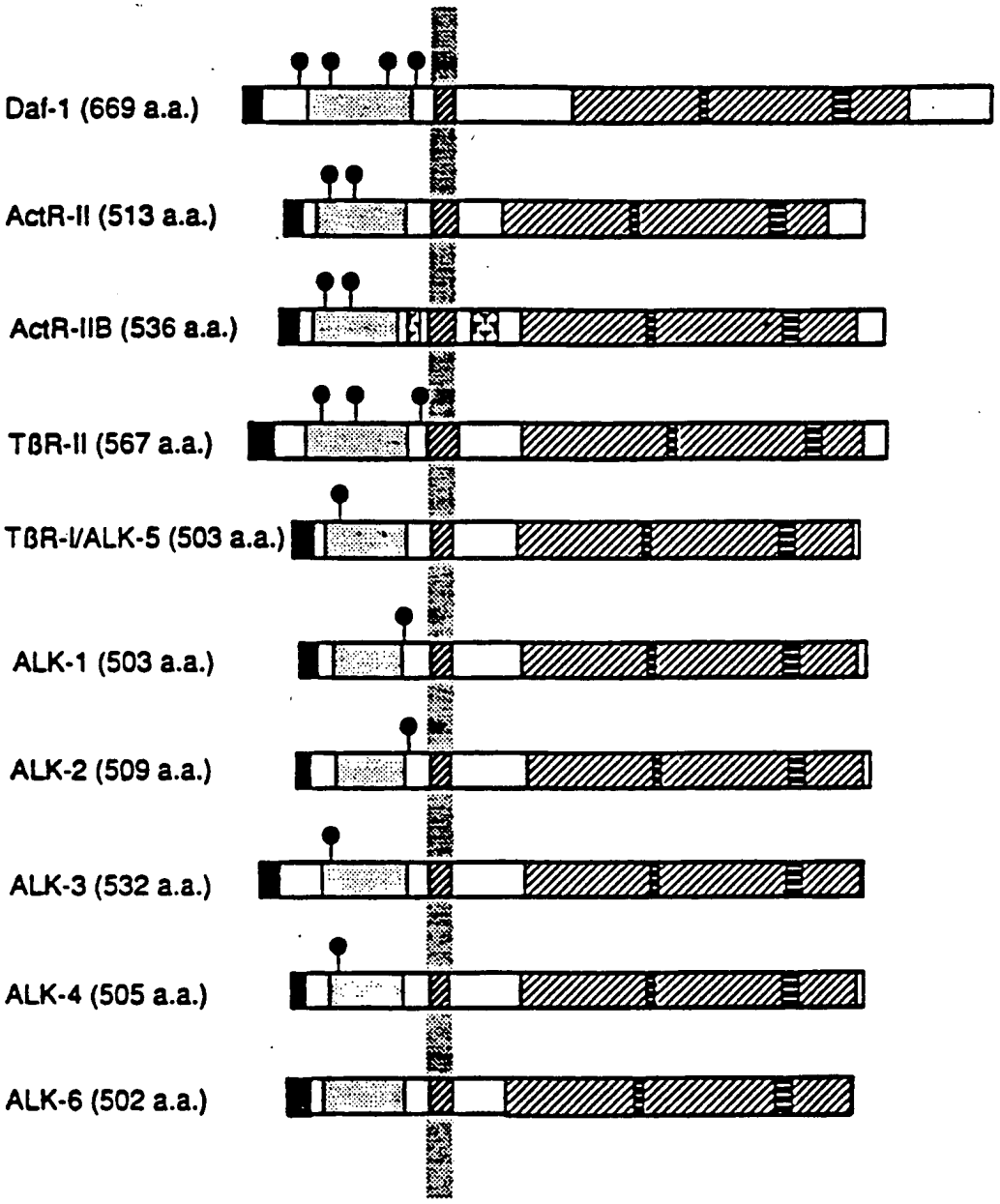
Daf-1 (669 a.a.)
ActR-II (513 a.a.)
ActR-IIB (536 a.a.)
TβR-II (567 a.a.)
TβR-I/ALK-5 (503 a.a.)
ALK-1 (503 a.a.)
ALK-2 (509 a.a.)
ALK-3 (532 a.a.)
ALK-4 (505 a.a.)
ALK-6 (502 a.a.)
signal sequence
cysteine-rich region
transmembrane domain
serine/threonine kinase domain
insert in the kinase domain
potential N-glycosylation site
alternatively spliced region

Fig. 4

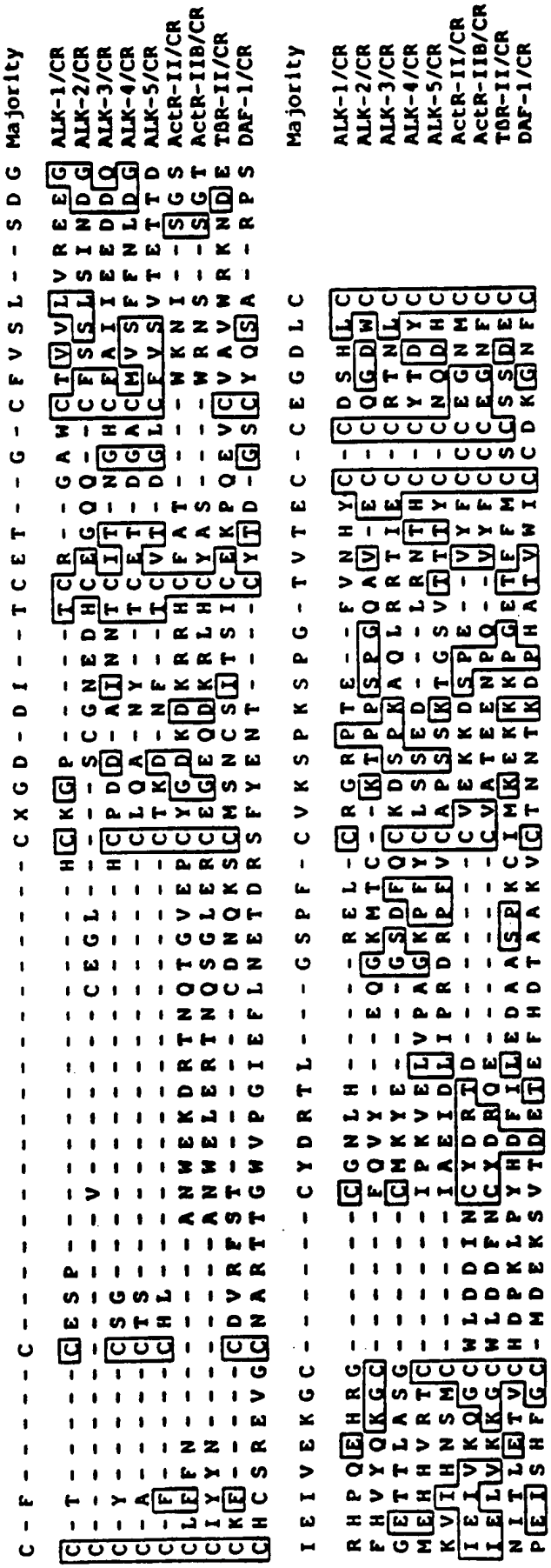
Majority
ALK-1/CR
ALK-2/CR
ALK-3/CR
ALK-4/CR
ALK-5/CR
ActR-II/CR
ActR-IIB/CR
TBR-II/CR
DAF-1/CR

Fig. 5

	ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TβR-II	daf-1
ALK-1	79	60	61	63	40	40	37	39
ALK-2		63	64	65	41	39	37	39
ALK-3			63	65	41	38	37	39
ALK-4				90	41	40	39	42
ALK-5					42	40	41	43
ActR-II						78	48	35
ActR-IIB							47	32
TβR-II								34

Fig. 6

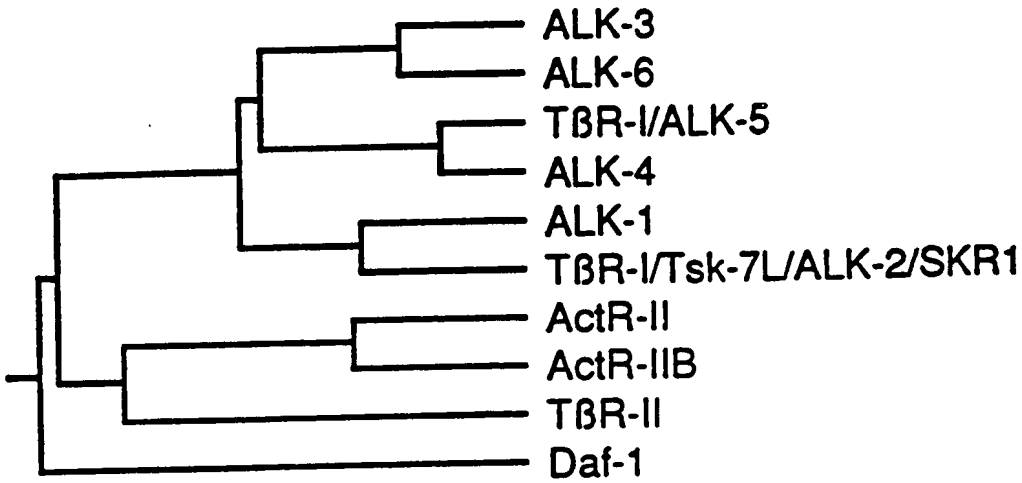
ALK-3
ALK-6
TβR-I/ALK-5
ALK-4
ALK-1
TβR-I/Tsk-7L/ALK-2/SKR1
ActR-II
ActR-IIB
TβR-II
Daf-1

Fig. 7